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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Mon Jun 11 13:25:27 EDT 2007

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\*\*\*\*\*

Reviewer Comments:

seq Id 6:

Missing amino acid numbering, they non-aligned 645,650,655

Please delete text appearing after seq id 21.

\*\*\*\*\*

Application No: 10813507 Version No: 2.0

Input Set:

Output Set:

**Started:** 2007-05-25 16:08:39.424  
**Finished:** 2007-05-25 16:08:48.098  
**Elapsed:** 0 hr(s) 0 min(s) 8 sec(s) 674 ms  
**Total Warnings:** 30  
**Total Errors:** 681  
**No. of SeqIDs Defined:** 21  
**Actual SeqID Count:** 21

| Error code | Error Description  |
|------------|--|
| W 112      | Upper case found in data; Found at position(0) SeqId(6)        |
| W 112      | Upper case found in data; Found at position(3) SeqId(6)        |
| W 112      | Upper case found in data; Found at position(6) SeqId(6)        |
| W 112      | Upper case found in data; Found at position(9) SeqId(6)        |
| W 112      | Upper case found in data; Found at position(12) SeqId(6)       |
| E 342      | 'n' position not defined found at POS: 15 SEQID(6)             |
| W 112      | Upper case found in data; Found at position(15) SeqId(6)       |
| W 112      | Upper case found in data; Found at position(18) SeqId(6)       |
| W 112      | Upper case found in data; Found at position(21) SeqId(6)       |
| W 112      | Upper case found in data; Found at position(24) SeqId(6)       |
| W 112      | Upper case found in data; Found at position(27) SeqId(6)       |
| W 112      | Upper case found in data; Found at position(30) SeqId(6)       |
| W 112      | Upper case found in data; Found at position(33) SeqId(6)       |
| W 112      | Upper case found in data; Found at position(36) SeqId(6)       |
| W 112      | Upper case found in data; Found at position(39) SeqId(6)       |
| W 112      | Upper case found in data; Found at position(42) SeqId(6)       |
| W 112      | Upper case found in data; Found at position(45) SeqId(6)       |
| E 323      | Invalid/missing amino acid numbering SEQID (6) POS (644)       |
| E 323      | Invalid/missing amino acid numbering SEQID (6)at Protein (645) |
| E 323      | Invalid/missing amino acid numbering SEQID (6) POS (649)       |

**Input Set:**

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| Error code | Error Description   |
|------------|---|
| E 323      | Invalid/missing amino acid numbering SEQID (6)at Protein (650)  |
| E 323      | Invalid/missing amino acid numbering SEQID (6) POS (654)  |
| E 323      | Invalid/missing amino acid numbering SEQID (6)at Protein (655)  |
| E 323      | Invalid/missing amino acid numbering SEQID (6) POS (659)  |
| E 323      | Invalid/missing amino acid numbering SEQID (6)at Protein (660)  |
| E 323      | Invalid/missing amino acid numbering SEQID (6) POS (664)  |
| E 323      | Invalid/missing amino acid numbering SEQID (6)at Protein (665)  |
| E 323      | Invalid/missing amino acid numbering SEQID (6) POS (669)  |
| E 323      | Invalid/missing amino acid numbering SEQID (6)at Protein (670)  |
| E 323      | Invalid/missing amino acid numbering SEQID (6) POS (674)  |
| E 323      | Invalid/missing amino acid numbering SEQID (6)at Protein (675)  |
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| E 323      | Invalid/missing amino acid numbering SEQID (6)at Protein (685)  |
| E 323      | Invalid/missing amino acid numbering SEQID (6) POS (689)  |
| E 323      | Invalid/missing amino acid numbering SEQID (6)at Protein (690)<br>This error has occurred more than 20 times, will not be displayed |
| E 331      | Count of Protein differs from the <211> tag Input: 2351<br>Calculated: 2335 SEQID(6)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (14)   |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (15)   |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (16)   |

**Input Set:**

**Output Set:**

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**Actual SeqID Count:** 21

| Error code | Error Description  |
|------------|--|
| W 213      | Artificial or Unknown found in <213> in SEQ ID (17)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (18)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (19)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (20)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (21)  |
| E 355      | Empty lines found between the amino acid numbering and the   |
| E 321      | No. of Bases conflict, this line has no nucleotides SEQID (21)   |
| E 355      | Empty lines found between the amino acid numbering and the   |
| E 321      | No. of Bases conflict, this line has no nucleotides SEQID (21)   |
| W 112      | Upper case found in data; Found at position(0) SeqId(21)   |
| W 112      | Upper case found in data; Found at position(1) SeqId(21)   |
| W 112      | Upper case found in data; Found at position(2) SeqId(21)   |
| W 112      | Upper case found in data; Found at position(14) SeqId(21)<br>This error has occurred more than 20 times, will not be displayed |

# SEQUENCE LISTING

<110> Lollar, John S.

<120> Nucleic Acid and Amino Acid Sequences  
encoding High-Level Expressor Factor VIII Polypeptides and  
Methods of Use

<130> 007157/ 276516

<140> 10813507

<141> 2004-03-30

<150> PCT/US02/33403

<151> 2002-10-07

<150> 60/327,388

<151> 2001-10-05

<160> 21

<170> FastSEQ for Windows Version 4.0

<210> 1

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<212> DNA

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<220>

<221> gene

<222> (1)...(6399)

<223> Factor VIII-- Full Length

<221> CDS

<222> (1)...(6399)

<400> 1

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| 1 5 10 15   |     |
| ggc ttt agt gcc atc agg aga tac tac ctg ggc gca gtg gaa ctg tcc | 96  |
| Gly Phe Ser Ala Ile Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser |     |
| 20 25 30  |     |
| tgg gac tac cgg caa agt gaa ctc ctc cgt gag ctg cac gtg gac acc | 144 |
| Trp Asp Tyr Arg Gln Ser Glu Leu Leu Arg Glu Leu His Val Asp Thr |     |
| 35 40 45  |     |
| aga ttt cct gct aca gcg cca gga gct ctt ccg ttg ggc ccg tca gtc | 192 |
| Arg Phe Pro Ala Thr Ala Pro Gly Ala Leu Pro Leu Gly Pro Ser Val |     |
| 50 55 60  |     |
| ctg tac aaa aag act gtg ttc gta gag ttc acg gat caa ctt ttc agc | 240 |
| Leu Tyr Lys Lys Thr Val Phe Val Glu Phe Thr Asp Gln Leu Phe Ser |     |
| 65 70 75 80   |     |

|   |     |
|---|-----|
| gtt gcc agg ccc agg cca cca tgg atg ggt ctg ctg ggt cct acc atc | 288 |
| Val Ala Arg Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile |     |
| 85 90 95  |     |
| cag gct gag gtt tac gac acg gtg gtc gtt acc ctg aag aac atg gct | 336 |
| Gln Ala Glu Val Tyr Asp Thr Val Val Thr Leu Lys Asn Met Ala     |     |
| 100 105 110   |     |
| tct cat ccc gtt agt ctt cac gct gtc ggc gtc tcc ttc tgg aaa tct | 384 |
| Ser His Pro Val Ser Leu His Ala Val Gly Val Ser Phe Trp Lys Ser |     |
| 115 120 125   |     |
| tcc gaa ggc gct gaa tat gag gat cac acc agc caa agg gag aag gaa | 432 |
| Ser Glu Gly Ala Glu Tyr Glu Asp His Thr Ser Gln Arg Glu Lys Glu |     |
| 130 135 140   |     |
| gac gat aaa gtc ctt ccc ggt aaa agc caa acc tac gtc tgg cag gtc | 480 |
| Asp Asp Lys Val Leu Pro Gly Lys Ser Gln Thr Tyr Val Trp Gln Val |     |
| 145 150 155 160   |     |
| ctg aaa gaa aat ggt cca aca gcc tct gac cca cca tgt ctc acc tac | 528 |
| Leu Lys Glu Asn Gly Pro Thr Ala Ser Asp Pro Pro Cys Leu Thr Tyr |     |
| 165 170 175   |     |
| tca tac ctg tct cac gtg gac ctg gtg aaa gac ctg aat tcg ggc ctc | 576 |
| Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu |     |
| 180 185 190   |     |
| att gga gcc ctg ctg gtt tgt aga gaa ggg agt ctg acc aga gaa agg | 624 |
| Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Thr Arg Glu Arg |     |
| 195 200 205   |     |
| acc cag aac ctg cac gaa ttt gta cta ctt ttt gct gtc ttt gat gaa | 672 |
| Thr Gln Asn Leu His Glu Phe Val Leu Leu Phe Ala Val Phe Asp Glu |     |
| 210 215 220   |     |
| ggg aaa agt tgg cac tca gca aga aat gac tcc tgg aca cgg gcc atg | 720 |
| Gly Lys Ser Trp His Ser Ala Arg Asn Asp Ser Trp Thr Arg Ala Met |     |
| 225 230 235 240   |     |
| gat ccc gca cct gcc agg gcc cag cct gca atg cac aca gtc aat ggc | 768 |
| Asp Pro Ala Pro Ala Arg Ala Gln Pro Ala Met His Thr Val Asn Gly |     |
| 245 250 255   |     |
| tat gtc aac agg tct ctg cca ggt ctg atc gga tgt cat aag aaa tca | 816 |
| Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Lys Lys Ser |     |
| 260 265 270   |     |
| gtc tac tgg cac gtg att gga atg ggc acc agc ccg gaa gtg cac tcc | 864 |
| Val Tyr Trp His Val Ile Gly Met Gly Thr Ser Pro Glu Val His Ser |     |
| 275 280 285   |     |
| att ttt ctt gaa ggc cac acg ttt ctc gtg agg cac cat cgc cag gct | 912 |
| Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg His His Arg Gln Ala |     |
| 290 295 300   |     |

|   |      |
|---|------|
| tcc ttg gag atc tcg cca cta act ttc ctc act gct cag aca ttc ctg | 960  |
| Ser Leu Glu Ile Ser Pro Leu Thr Phe Leu Thr Ala Gln Thr Phe Leu |      |
| 305 310 315 320   |      |
| atg gac ctt ggc cag ttc cta ctg ttt tgt cat atc tct tcc cac cac | 1008 |
| Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His His |      |
| 325 330 335   |      |
| cat ggt ggc atg gag gct cac gtc aga gta gaa agc tgc gcc gag gag | 1056 |
| His Gly Gly Met Glu Ala His Val Arg Val Glu Ser Cys Ala Glu Glu |      |
| 340 345 350   |      |
| ccc cag ctg cgg agg aaa gct gat gaa gag gaa gat tat gat gac aat | 1104 |
| Pro Gln Leu Arg Arg Lys Ala Asp Glu Glu Glu Asp Tyr Asp Asp Asn |      |
| 355 360 365   |      |
| ttg tac gac tcg gac atg gac gtg gtc cgg ctc gat ggt gac gac gtg | 1152 |
| Leu Tyr Asp Ser Asp Met Asp Val Val Arg Leu Asp Gly Asp Asp Val |      |
| 370 375 380   |      |
| tct ccc ttt atc caa atc cgc tcg gtt gcc aag aag cat ccc aaa acc | 1200 |
| Ser Pro Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr |      |
| 385 390 395 400   |      |
| tgg gtg cac tac atc tct gca gag gag gag gac tgg gac tac gcc ccc | 1248 |
| Trp Val His Tyr Ile Ser Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro |      |
| 405 410 415   |      |
| gcg gtc ccc agc ccc agt gac aga agt tat aaa agt ctc tac ttg aac | 1296 |
| Ala Val Pro Ser Pro Ser Asp Arg Ser Tyr Lys Ser Leu Tyr Leu Asn |      |
| 420 425 430   |      |
| agt ggt cct cag cga att ggt agg aaa tac aaa aaa gct cga ttc gtc | 1344 |
| Ser Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Ala Arg Phe Val |      |
| 435 440 445   |      |
| gct tac acg gat gta aca ttt aag act cgt aaa gct att ccg tat gaa | 1392 |
| Ala Tyr Thr Asp Val Thr Phe Lys Thr Arg Lys Ala Ile Pro Tyr Glu |      |
| 450 455 460   |      |
| tca gga atc ctg gga cct tta ctt tat gga gaa gtt gga gac aca ctt | 1440 |
| Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu |      |
| 465 470 475 480   |      |
| ttg att ata ttt aag aat aaa gcg agc cga cca tat aac atc tac cct | 1488 |
| Leu Ile Ile Phe Lys Asn Lys Ala Ser Arg Pro Tyr Asn Ile Tyr Pro |      |
| 485 490 495   |      |
| cat gga atc act gat gtc agc gct ttg cac cca ggg aga ctt cta aaa | 1536 |
| His Gly Ile Thr Asp Val Ser Ala Leu His Pro Gly Arg Leu Leu Lys |      |
| 500 505 510   |      |
| ggt tgg aaa cat ttg aaa gac atg cca att ctg cca gga gag act ttc | 1584 |
| Gly Trp Lys His Leu Lys Asp Met Pro Ile Leu Pro Gly Glu Thr Phe |      |
| 515 520 525   |      |
| aag tat aaa tgg aca gtg act gtg gaa gat ggg cca acc aag tcc gat | 1632 |

|   |      |
|---|------|
| Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp |      |
| 530 535 540   |      |
| cct cgg tgc ctg acc cgc tac tac tcg agc tcc att aat cta gag aaa | 1680 |
| Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Ile Asn Leu Glu Lys     |      |
| 545 550 555 560   |      |
| gat ctg gct tcg gga ctc att ggc cct ctc ctc atc tgc tac aaa gaa | 1728 |
| Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu |      |
| 565 570 575   |      |
| tct gta gac caa aga gga aac cag atg atg tca gac aag aga aac gtc | 1776 |
| Ser Val Asp Gln Arg Gly Asn Gln Met Met Ser Asp Lys Arg Asn Val |      |
| 580 585 590   |      |
| atc ctg ttt tct gta ttc gat gag aat caa agc tgg tac ctc gca gag | 1824 |
| Ile Leu Phe Ser Val Phe Asp Glu Asn Gln Ser Trp Tyr Leu Ala Glu |      |
| 595 600 605   |      |
| aat att cag cgc ttc ctc ccc aat ccg gat gga tta cag ccc cag gat | 1872 |
| Asn Ile Gln Arg Phe Leu Pro Asn Pro Asp Gly Leu Gln Pro Gln Asp |      |
| 610 615 620   |      |
| cca gag ttc caa gct tct aac atc atg cac agc atc aat ggc tat gtt | 1920 |
| Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val |      |
| 625 630 635 640   |      |
| ttt gat agc ttg cag ctg tcg gtt tgt ttg cac gag gtg gca tac tgg | 1968 |
| Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp |      |
| 645 650 655   |      |
| tac att cta agt gtt gga gca cag acg gac ttc ctc tcc gtc ttc ttc | 2016 |
| Tyr Ile Leu Ser Val Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe |      |
| 660 665 670   |      |
| tct ggc tac acc ttc aaa cac aaa atg gtc tat gaa gac aca ctc acc | 2064 |
| Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr |      |
| 675 680 685   |      |
| ctg ttc ccc ttc tca gga gaa acg gtc ttc atg tca atg gaa aac cca | 2112 |
| Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro |      |
| 690 695 700   |      |
| ggg ctc tgg gtc cta ggg tgc cac aac tca gac ttg cgg aac aga ggg | 2160 |
| Gly Leu Trp Val Leu Gly Cys His Asn Ser Asp Leu Arg Asn Arg Gly |      |
| 705 710 715 720   |      |
| atg aca gcc tta ctg aag gtg tat agt tgt gac agg gac att ggt gat | 2208 |
| Met Thr Ala Leu Leu Lys Val Tyr Ser Cys Asp Arg Asp Ile Gly Asp |      |
| 725 730 735   |      |
| tat tat gac aac act tat gaa gat att cca ggc ttc ttg ctg agt gga | 2256 |
| Tyr Tyr Asp Asn Thr Tyr Glu Asp Ile Pro Gly Phe Leu Leu Ser Gly |      |
| 740 745 750   |      |
| aag aat gtc att gaa ccc aga agc ttt gcc cag aat tca aga ccc cct | 2304 |
| Lys Asn Val Ile Glu Pro Arg Ser Phe Ala Gln Asn Ser Arg Pro Pro |      |



| 755   | 760 | 765 |      |
|---|-----|-----|------|
| agt gcg agc caa aag caa ttc caa acc atc aca agt cca gaa gat gac |     |     | 2352 |
| Ser Ala Ser Gln Lys Gln Phe Gln Thr Ile Thr Ser Pro Glu Asp Asp |     |     |      |
| 770   | 775 | 780 |      |
| gtg gag ctt gac ccg cag tct gga gag aga acc caa gca ctg gaa gaa |     |     | 2400 |
| Val Glu Leu Asp Pro Gln Ser Gly Glu Arg Thr Gln Ala Leu Glu Glu |     |     |      |
| 785   | 790 | 795 | 800  |
| cta agt gtc ccc tct ggt gat ggg tcg atg ctc ttg gga cag aat cct |     |     | 2448 |
| Leu Ser Val Pro Ser Gly Asp Gly Ser Met Leu Leu Gly Gln Asn Pro |     |     |      |
|   | 805 | 810 | 815  |
| gct cca cat ggc tca tcc tca tct gat ctt caa gaa gcc agg aat gag |     |     | 2496 |
| Ala Pro His Gly Ser Ser Ser Ser Asp Leu Gln Glu Ala Arg Asn Glu |     |     |      |
|   | 820 | 825 | 830  |
| gct gat gat tat tta cct gga gca aga gaa aga ggc acg gcc cca tcc |     |     | 2544 |
| Ala Asp Asp Tyr Leu Pro Gly Ala Arg Glu Arg Gly Thr Ala Pro Ser |     |     |      |
|   | 835 | 840 | 845  |
| gca gcg gca cgt ctc aga cca gag ctg cat cac agt gcc gaa aga gta |     |     | 2592 |
| Ala Ala Ala Arg Leu Arg Pro Glu Leu His His Ser Ala Glu Arg Val |     |     |      |
|   | 850 | 855 | 860  |
| ctt act cct gag cca gag aaa gag ttg aag aaa ctt gat tca aaa atg |     |     | 2640 |
| Leu Thr Pro Glu Pro Glu Lys Glu Leu Lys Lys Leu Asp Ser Lys Met |     |     |      |
| 865   | 870 | 875 | 880  |
| tct agt tca tca gac ctt cta aag act tcg cca aca att cca tca gac |     |     | 2688 |
| Ser Ser Ser Ser Asp Leu Leu Lys Thr Ser Pro Thr Ile Pro Ser Asp |     |     |      |
|   | 885 | 890 | 895  |
| acg ttg tca gcg gag act gaa agg aca cat tcc tta ggc ccc cca cac |     |     | 2736 |
| Thr Leu Ser Ala Glu Thr Glu Arg Thr His Ser Leu Gly Pro Pro His |     |     |      |
|   | 900 | 905 | 910  |
| ccg cag gtt aat ttc agg agt caa tta ggt gcc att gta ctt ggc aaa |     |     | 2784 |
| Pro Gln Val Asn Phe Arg Ser Gln Leu Gly Ala Ile Val Leu Gly Lys |     |     |      |
|   | 915 | 920 | 925  |
| aat tca tct cac ttt att ggg gct ggt gtc cct ttg ggc tcg act gag |     |     | 2832 |
| Asn Ser Ser His Phe Ile Gly Ala Gly Val Pro Leu Gly Ser Thr Glu |     |     |      |
|   | 930 | 935 | 940  |
| gag gat cat gaa agc tcc ctg gga gaa aat gta tca cca gtg gag agt |     |     | 2880 |
| Glu Asp His Glu Ser Ser Leu Gly Glu Asn Val Ser Pro Val Glu Ser |     |     |      |
| 945   | 950 | 955 | 960  |
| gac ggg ata ttt gaa aag gaa aga gct cat gga cct gct tca ctg acc |     |     | 2928 |
| Asp Gly Ile Phe Glu Lys Glu Arg Ala His Gly Pro Ala Ser Leu Thr |     |     |      |
|   | 965 | 970 | 975  |
| aaa gac gat gtt tta ttt aaa gtt aat atc tct ttg gta aag aca aac |     |     | 2976 |
| Lys Asp Asp Val Leu Phe Lys Val Asn Ile Ser Leu Val Lys Thr Asn |     |     |      |
|   | 980 | 985 | 990  |

|   |      |
|---|------|
| aag gca cga gtt tac tta aaa act aat aga aag att cac att gat gac | 3024 |
| Lys Ala Arg Val Tyr Leu Lys Thr Asn Arg Lys Ile His Ile Asp Asp |      |
| 995 1000 1005   |      |
| gca gct tta tta act gag aat agg gca tct gca acg ttt atg gac aaa | 3072 |
| Ala Ala Leu Leu Thr Glu Asn Arg Ala Ser Ala Thr Phe Met Asp Lys |      |
| 1010 1015 1020  |      |
| aat act aca gct tcg gga tta aat cat gtg tca aat tgg ata aaa ggg | 3120 |
| Asn Thr Thr Ala Ser Gly Leu Asn His Val Ser Asn Trp Ile Lys Gly |      |
| 1025 1030 1035 1040   |      |
| ccc ctt ggc aag aac ccc cta agc tcg gag cga ggc ccc agt cca gag | 3168 |
| Pro Leu Gly Lys Asn Pro Leu Ser Ser Glu Arg Gly Pro Ser Pro Glu |      |
| 1045 1050 1055  |      |
| ctt ctg aca tct tca gga tca gga aaa tct gtg aaa ggt cag agt tct | 3216 |
| Leu Leu Thr Ser Ser Gly Ser Gly Lys Ser Val Lys Gly Gln Ser Ser |      |
| 1060 1065 1070  |      |
| ggg cag ggg aga ata cgg gtg gca gtg gaa gag gaa gaa ctg agc aaa | 3264 |
| Gly Gln Gly Arg Ile Arg Val Ala Val Glu Glu Glu Glu Leu Ser Lys |      |
| 1075 1080 1085  |      |
| ggc aaa gag atg atg ctt ccc aac agc gag ctc acc ttt ctc act aac | 3312 |
| Gly Lys Glu Met Met Leu Pro Asn Ser Glu Leu Thr Phe Leu Thr Asn |      |
| 1090 1095 1100  |      |
| tcg gct gat gtc caa gga aac gat aca cac agt caa gga aaa aag tct | 3360 |
| Ser Ala Asp Val Gln Gly Asn Asp Thr His Ser Gln Gly Lys Lys Ser |      |
| 1105 1110 1115 1120   |      |
| cgg gaa gag atg gaa agg aga gaa aaa tta gtc caa gaa aaa gtc gac | 3408 |
| Arg Glu Glu Met Glu Arg Arg Glu Lys Leu Val Gln Glu Lys Val Asp |      |
| 1125 1130 1135  |      |
| ttg cct cag gtg tat aca gcg act gga act aag aat ttc ctg aga aac | 3456 |
| Leu Pro Gln Val Tyr Thr Ala Thr Gly Thr Lys Asn Phe Leu Arg Asn |      |
| 1140 1145 1150  |      |
| att ttt cac caa agc act gag ccc agt gta gaa ggg ttt gat ggg ggg | 3504 |
| Ile Phe His Gln Ser Thr Glu Pro Ser Val Glu Gly Phe Asp Gly Gly |      |
| 1155 1160 1165  |      |
| tca cat gcg ccg gtg cct caa gac agc agg tca tta aat gat tcg gca | 3552 |
| Ser His Ala Pro Val Pro Gln Asp Ser Arg Ser Leu Asn Asp Ser Ala |      |
| 1170 1175 1180  |      |
| gag aga gca gag act cac ata gcc cat ttc tca gca att agg gaa gag | 3600 |
| Glu Arg Ala Glu Thr His Ile Ala His Phe Ser Ala Ile Arg Glu Glu |      |
| 1185 1190 1195 1200   |      |
| gca ccc ttg gaa gcc ccg gga aat cga aca ggt cca ggt ccg agg agt | 3648 |
| Ala Pro Leu Glu Ala Pro Gly Asn Arg Thr Gly Pro Gly Pro Arg Ser |      |
| 1205 1210 1215  |      |

|   |      |
|---|------|
| gcg gtt ccc cgc cgc gtt aag cag agc ttg aaa cag atc aga ctc ccg | 3696 |
| Ala Val Pro Arg Arg Val Lys Gln Ser Leu Lys Gln Ile Arg Leu Pro |      |
| 1220 1225 1230  |      |
| cta gaa gaa ata aag cct gaa agg ggg gtg gtt ctg aat gcc acc tca | 3744 |
| Leu Glu Glu Ile Lys Pro Glu Arg Gly Val Val Leu Asn Ala Thr Ser |      |
| 1235 1240 1245  |      |
| acc cgg tgg tct gaa agc agt cct atc tta caa gga gcc aaa aga aat | 3792 |
| Thr Arg Trp Ser Glu Ser Ser Pro Ile Leu Gln Gly Ala Lys Arg Asn |      |
| 1250 1255 1260  |      |
| aac ctt tct tta cct ttc ctg acc ttg gaa atg gcc gga ggt caa gga | 3840 |
| Asn Leu Ser Leu Pro Phe Leu Thr Leu Glu Met Ala Gly Gly Gln Gly |      |
| 1265 1270 1275 1280   |      |
| aag atc agc gcc ctg ggg aaa agt gcc gca ggc ccg ctg gcg tcc ggg | 3888 |
| Lys Ile Ser Ala Leu Gly Lys Ser Ala Ala Gly Pro Leu Ala Ser Gly |      |
| 1285 1290 1295  |      |
| aag ctg gag aag gct gtt ctc tct tca gca ggc ttg tct gaa gca tct | 3936 |
| Lys Leu Glu Lys Ala Val Leu Ser Ser Ala Gly Leu Ser Glu Ala Ser |      |
| 1300 1305 1310  |      |
| ggc aaa gct gag ttt ctt cct aaa gtt cga gtt cat cgg gaa gac ctg | 3984 |
| Gly Lys Ala Glu Phe Leu Pro Lys Val Arg Val His Arg Glu Asp Leu |      |
| 1315 1320 1325  |      |
| ttg cct caa aaa acc agc aat gtt tct tgc gca cac ggg gat ctc ggc | 4032 |
| Leu Pro Gln Lys Thr Ser Asn Val Ser Cys Ala His Gly Asp Leu Gly |      |
| 1330 1335 1340  |      |
| cag gag atc ttc ctg cag aaa aca cgg gga cct gtt aac ctg aac aaa | 4080 |
| Gln Glu Ile Phe Leu Gln Lys Thr Arg Gly Pro Val Asn Leu Asn Lys |      |
| 1345 1350 1355 1360   |      |
| gta aat aga cct gga agg act ccc tcc aag ctt ctg ggt ccc ccg atg | 4128 |
| Val Asn Arg Pro Gly Arg Thr Pro Ser Lys Leu Leu Gly Pro Pro Met |      |
| 1365 1370 1375  |      |
| ccc aaa gag tgg gaa tcc cta gag aag tca cca aaa agc aca gct ctc | 4176 |
| Pro Lys Glu Trp Glu Ser Leu Glu Lys Ser Pro Lys Ser Thr Ala Leu |      |
| 1380 1385 1390  |      |
| agg acg aaa gac atc atc agt tta ccc ctg gac cgt cac gaa agc aat | 4224 |